


```

RESULT 2
ID E311_ADE06 STANDARD; PRT: 101 AA.
AC 055653;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early E3A 11.6 kDa glycoprotein.
OS Human adenovirus type 6.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10534;
[1]
RP SEQUENCE FROM N.A.
RA Reichmann H., Schaarschmidt E., Geiseler B., Hausmann J., Ortman D.,
RA Bauer U., Flunker G., Seidel W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.
CC -1- PTM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER AD2 E3A 11.6
CC kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.
CC -----
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CC -----
CC EMBL: Y16037; CAA75991.1;
CC DR Early protein; Glycoprotein; Transmembrane.
CC KW TRANSMEM 41 62 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT CARBOHYD 14 14
CC FT SEQUENCE 101 AA; 11613 MW; E219000935E3B4B CRC64;
CC SQ

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Query Match 39.0%; Score 30; DB 1; Length 101;
 Best Local Similarity 100.0%; Pred. No. 1.5e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 41 MMFSTALMFVCLIMLWICLRRARRP 70
DB 41 MMFSTALMFVCLIMLWICLRRARRP 70

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```

RESULT 3
ID E311_ADE05 STANDARD; PRT: 93 AA.
AC P17590;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Early E3A 10.5 kDa glycoprotein.
OS Human adenovirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=28285;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85092386; PubMed=2981456;
RA Cladars C., Mold W.S.M.;
RT "DNA sequence of the early E3 transcription unit of adenovirus 5.";
RL Virology 140:28-43(1985).
[2]
RN COMPLETE GENOME.
RP MEDLINE=92087470; PubMed=1727603;
RX Chroboczek J., Bieker F., Jacrot B.;
RT "The sequence of the genome of adenovirus type 5 and its comparison
RT with the genome of adenovirus type 2.";
RL Virology 186:280-285(1992).
CC -1- SUBCELLULAR LOCATION: INTEGRAL NUCLEAR MEMBRANE PROTEIN.
CC -1- PTM: N-GLYCOSYLATED AND PROBABLY ALSO O-GLYCOSYLATED.

```

```

CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER AD2 E3A 11.6
CC kDa, AD5 E3A 10.5 kDa, AD3 E3 9 kDa, AND AD7 E3 7.7 kDa.
CC -----
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CC -----
CC EMBL: M73260; NOT ANNOTATED_CDS.
CC DR EMBL: X03002; CAA26784.1;
CC DR PIR: A05245; ERA053.
CC KW Early protein; Glycoprotein; Transmembrane.
CC FT TRANSMEM 34 35
CC FT CARBOHYD 3 3 N-LINKED (GLCNAC... ) (POTENTIAL).
CC FT SEQUENCE 93 AA; 10523 MW; 008AD087AD45A8F CRC64;
CC SQ

```

Query Match 31.2%; Score 24; DB 1; Length 93;
 Best Local Similarity 100.0%; Pred. No. 2.8e-18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 41 MMFSTALMFVCLIMLWICLRR 64
DB 34 MMFSTALMFVCLIMLWICLRR 57

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RESULT 4
ID ATP8_ORNAN STANDARD; PRT: 69 AA.
AC Q36453;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN ATP8 OR ATP8
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Mithochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
NCBI_TaxID=9258;
[1]
RP SEQUENCE FROM N.A.
RA TISSUE=Heart, and Liver;
RX MEDLINE=97077300; PubMed=8919867;
RA Janke A., Gemmell N., Feldmaler-Fuchs G., von Haeseler A.;
RA Paabo S.;
RT "The mitochondrial genome of a monotreme -- the platypus
RT (Ornithorhynchus anatinus).";
RL J. Mol. Evol. 42:153-159(1996).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF0) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC -----
CC EMBL: X83427; CAA58459.1;
CC DR InterPro: IPR001421; ATP-synt_8.
CC DR InterPro: IPR003236; Mamm_mito_ATPase_8.
CC DR Pfam: PF00895; ATP-synt_8; 1.
CC DR ProDom: PD001090; Mamm_mito_ATPase_8; 1.
CC KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
CC FT TRANSMEM 8 24
CC FT SEQUENCE 69 AA; 8288 MW; B704FDA339643C20 CRC64;
CC SQ

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OY 69 PSLILO 75
 DB 1024 PSLILO 1030

RESULT 7

HRK_MOUSE STANDARD: PRT: 92 AA.
 ID HRK_MOUSE
 AC P70678;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Activator of apoptosis harkiri (Neuronal death protein DP5).
 GN Hrk or DP5 or BID.
 OS Mus musculus (Mouse), and
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090, 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Imai et al. K. I.
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTIVATES APOPTOSIS AND INTERACTS SELECTIVELY WITH
 CC SURVIVAL-PROMOTING PROTEINS BCL-2 AND BCL-XL (BY SIMILARITY).
 CC -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR THE INDUCTION OF CELL
 CC DEATH (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
 CC -----
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 CC -----
 CC DR EMBL; D83697; BAA12065.1; -;
 CC DR EMBL; D83698; BAA12066.1; -;
 CC DR MGD; MGI:1201608; B1d3.
 CC DR InterPro; IPR000712; BCL_2.
 CC DR PROSITE; PS01255; BH3_1.
 CC KW Apoptosis.
 CC FT DOMAIN 33 47 BH3.
 CC FT SEQUENCE 92 AA; 10078 MW; 95760B9E8A8F1DE CRC64;

Query Match 7.8%; Score 6; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 69
 DB 50 RRRARP 55

RESULT 8

VNRP_POPPV STANDARD: PRT: 121 AA.
 ID VNRP_POPPV
 AC 002123;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE 14 kDa protein (putative nucleic acid-binding protein).
 OS Poplar mosaic virus (Isolate ATCC PV275) (PMV).
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
 CC NCBI_TaxID=31709;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9233381; PubMed=1629709;
 RA Henderson J., Gibbs M.J., Edwards M.L., Clarke V.A., Gardner K.A.,

RA Cooper J.I.;
 RT "Partial nucleotide sequence of poplar mosaic virus RNA confirms its
 RT classification as a Carlavirus.";
 RL J. Gen. Virol. 73:1887-1890 (1992).
 CC -1- FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
 CC TRANSCRIPTION.
 CC -1- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER
 CC CARLAVIRUSES.
 CC -----

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 CC -----

DR EMBL; X65102; CA46227.1; -;
 DR EMBL; D13364; BAA02629.1; -;
 DR PIR; J01646; J01646.
 DR PIR; S23876; S23876.
 DR InterPro; IPR002568; Carla_C4.
 DR Pfam; PF01623; Carla_C4_1.
 DR Pfam; PF01623; Carla_C4_1.
 DR ZN-Finger; 62 83 C4-TYPE (POTENTIAL).
 FT ZN-Finger 62 83
 FT SEQUENCE 121 AA; 14451 MW; 70520527BF7D3CF CRC64;

Query Match 7.8%; Score 6; DB 1; Length 121;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 RRRARP 68
 DB 52 RRRARP 57

RESULT 9

NIFW_FRASE STANDARD: PRT: 126 AA.
 ID NIFW_FRASE
 AC Q92510;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Nitrogenase stabilizing/protective protein, nifw.
 GN Nifw.
 OS Frankia sp. (strain Eu1K1).
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Frankiaceae; Frankia.
 CC NCBI_TaxID=47227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Eu1K1;
 RA Chung-Sun A., Ji-Tee K., Won-Jin K., Won-Young Y.;
 RT "Nif-gene organization and nucleotide sequences from Frankia Eu1K1
 RT strain.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative
 CC damage (by similarity).
 CC -1- SUBUNIT: Homotrimer; associates with nifD (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE NIFW FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; AF119361; AADI7267.1; -;
 KW Nitrogen fixation.
 SO SEQUENCE 126 AA; 14287 MW; 295D8C9102FD317E CRC64;

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Oy      15  TTAGGL 20
Db      80  TTAGGL 85

RESULT 10
ID      YRNG.CAEEL      STANDARD:      PRT: 136 AA.
AC      009420:
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      Hypothetical 14.2 kDa protein R07B1.6 in chromosome X.
GN      R07B1.6.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
Ox      Rhabditidae; Pelodierinae; Caenorhabditis.
Ox      NCBI_TaxId=6239;
Ox      [1]
Ox      SEQUENCE FROM N.A.
Ox      STRAIN=BRISTOL NZ;
Ox      Kershaw J.;
Ox      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
Ox      -----
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Ox      -----
Ox      DR      EMBL: Z48631; CA88543.1; -
Ox      DR      WormPep: R07B1.6; CE01632.
Ox      DR      InterPro: IPR002601; C6.
Ox      DR      Pfam: PF01681; C6; 1.
Ox      KW      Hypothetical protein.
Ox      SQ      SEQUENCE 136 AA; 14169 MW; D7F47A83F3F81787 CRC64;
Ox      -----

Query Match
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5  TIAPTT 10
Db      31  TIAPTT 36

RESULT 11
ID      YB9E.YEAST      STANDARD:      PRT: 142 AA.
AC      P3837;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Hypothetical 16.4 kDa protein in POP-1/SH1 Intergenic region.
GN      YBR258C OR YBR1726.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Ox      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Ox      NCBI_TaxId=4932;
Ox      [1]
Ox      SEQUENCE FROM N.A.
Ox      STRAIN=S288C;
Ox      MEDLINE=93220397; PubMed=8455606;
Ox      Dolignon F.; Bileau N.; Crouzet M.; Aigle M.;

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RT      "The complete sequence of a 19,482 bp segment located on the right
RT      arm of chromosome II from Saccharomyces cerevisiae."
RL      Yeast 9:189-199(1993).
CC      -----
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CC      -----
DR      EMBL: X70529; CAA49922.1; -
DR      EMBL: Z36127; CAA85221.1; -
DR      PIR: S32960; S32960.
DR      SGD: S0000462; YBR258C.
KW      Hypothetical protein.
SQ      SEQUENCE 142 AA; 16429 MW; 12E73F0C3DD225D7 CRC64;
OY      19 GLTSL 24
Db      71 GLTSL 76
RESULT 12
YC61_MYCTU
ID      YC61_MYCTU          STANDARD;          PRT;          149 AA.
AC      011057;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical 16.8 kDa protein RV1261C.
DE      RV1261C OR MW1299 OR MTCY50.21.
OS      Mycobacterium tuberculosis.
OC      Bacteria; Filicutes; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX      NCBI_TaxID=1773;
RN      11]
RP      SEQUENCE FROM N.A.
RC      STRAIN=H37RV;
RC      MEDLINE=98295987; PubMed=9634230;
RX      Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA      Cole S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA      Davies K., Basham D., Brown D., Chillingworth T., Connor R.,
RA      Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA      Hornsby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,
RA      Oliver S., Osborne J., Quail M.A., Ralston J.M., Rogers J.,
RA      Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA      Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT      "Deciphering the biology of Mycobacterium tuberculosis from the
RT      complete genome sequence."
RL      Nature 393:537-544(1998).
RL      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CDC 1551 / Oshkosh;
RC      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA      Peterson J., Deboy R., Dodson R., Gaitan M.L., Haft D., Hickey E.,
RA      Kolonay J.F., Nelson W.C., Umayam L.A., Emolaeve M.D., Salzberg S.L.,
RA      Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA      Bishai W.;
RT      "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT      laboratory strains."
RT      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC      1- SIMILARITY: TO M.TUBERCULOSIS RV1558.
CC      -----
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CC -----
DR EMBL: 277137; CAB00892.1; .
DR EMBL: A6007005; AAK45558.1; .
DR TIGR: W1299; .
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 149 AA; 16756 MW; D8F22A51B5F43FCF CRC64;

Query Match 7.8%; Score 6; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 PPSLL 74
DB 38 PPSLL 43

RESULT 13
RK34_SPTOL STANDARD: PRT; 152 AA.
ID RK34_SPTOL
AC P82244;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE 50S ribosomal protein L34, chloroplast precursor.
GN RPL34.
OS Spinacia oleracea (Spinach).
CC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Caryophyllales; Caryophyllales; Chenopodiales; Spinacia.
CC NCBI_TaxID=562;
CC [1]
CC SEQUENCE FROM N.A., SEQUENCE OF 92-101, AND MASS SPECTROMETRY.
RP STRAIN=CY. ALMARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamauchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- TISSUE SPECIFICITY: UBICUITOUS.
CC -1- MASS SPECTROMETRY: MW=6767.1; METHOD=Electrospray; RANGE=92-152.
CC -1- SIMILARITY: BELONGS TO THE L34P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: AF38221; AAF64157.1; .
DR InterPro: IPR00271; Ribosomal_L34.
DR Pfam: PF00468; Ribosomal_L34; 1.
DR PROSITE: PS00784; Ribosomal_L34; FALSE NEG.
KW Ribosomal protein; Chloroplast; Transit peptide; rRNA-binding.
FT TRANSIT 1 91 CHLOROPLAST.
FT CHAIN 92 152 50S RIBOSOMAL PROTEIN L34.
SQ SEQUENCE 152 AA; 16095 MW; 755A990D41ADB18 CRC64;

Query Match 7.8%; Score 6; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LKRRRA 67

DB 127 LKRRRA 132

RESULT 14
HES2_MOUSE STANDARD: PRT; 157 AA.
ID HES2_MOUSE
AC 054792;
DT 15-DEC-1998 (Rel. 37; Created)
DT 15-DEC-1998 (Rel. 37; Last sequence update)
DT 15-DEC-1998 (Rel. 37; Last annotation update)
DE Transcription factor HES-2 (Hairy and enhancer of split 2).
GN HES2.
OS Mus musculus (Mouse).
CC Eukaryote; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
RP STRAIN=129/3;
RX MEDLINE=98234545; PubMed=9570950;
RA Nishimura M., Isaka F., Ishibashi M., Tomita K., Tsuda H.,
RA Nakanishi S., Kageyama R.;
RT "Structure, chromosomal locus, and promoter of mouse Hes2 gene, a
RT homologue of Drosophila hairy and enhancer of split.";
RT Genomics 49:69-75(1998).
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
CC PROTEIN FOR THEIR TRANSCRIPTION.
CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX
CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).
CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
CC RATHER THAN THE CANONICAL E-BOX (CANNTG).
CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRWP MOTIF IS A TRANSCRIPTIONAL
CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
CC HAIRY-RELATED PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
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CC -----
DR EMBL: AB009967; BAA24091.1; .
DR MGI: 1098624; Hes2.
DR InterPro: IPR003015; HLH_MYC.
DR InterPro: IPR001092; HLH_dlm.
DR InterPro: IPR003650; Orange.
DR Pfam: PF00010; HLH; 1.
DR SMART: SM00353; HLH; 1.
DR SMART: SM00511; ORANGE; 1.
DR Transcription regulation; DNA-binding; Nuclear protein; Repressor.
KW Transcription regulation; DNA-binding; Nuclear protein; Repressor.
FT DNA_BIND 13 26 BASIC DOMAIN.
FT DOMAIN 27 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 139 148 PRO-RICH.
FT DOMAIN 154 157 WRWP MOTIF (REQUIRED FOR ACTIVITY)
FT DOMAIN (BY SIMILARITY).
SQ SEQUENCE 157 AA; 17231 MW; 570A0C67F4992EA7 CRC64;

Query Match 7.8%; Score 6; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 63 KRRRAR 68
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DB 23 KRRRAR 28

DB 23 KRRRAR 28

Search completed: June 21, 2002, 08:25:26
Job time: 311 sec

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RESULT 15
HES2_RAT STANDARD: PRT: 157 AA.
AC P35429;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Transcription factor HES-2 (Hairy and enhancer of split 2).
GN HES2 OR HES-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic brain;
RX MEDLINE=9335886; PubMed=8354270;
RA Ishibashi M., Sasai Y., Nakanishi S., Kagayama R.;
RT Molecular characterization of HES-2, a mammalian helix-loop-helix
RT factor structurally related to Drosophila hairy and Enhancer of
RT split.
RT Eur. J. Biochem. 215:645-652(1993).
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
CC PROTEIN FOR THEIR TRANSCRIPTION.
CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX
CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CANCNG),
CC RATHER THAN THE CANONICAL E-BOX (CANNNG).
CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL
CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
CC HAIRY-RELATED PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D14029; BAA03118.1; -
DR PIR: S35037; S35037.
DR TRANSPAC: T01650; -
DR InterPro: IPR003015; HLH_Myc.
DR InterPro: IPR001092; HLH_dim.
DR InterPro: IPR003650; Orange.
DR Pfam: PF00010; HLH.1.
DR SMART: SM00353; HLH.1.
DR SMART: SM00511; ORANGE.1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX.1.
KW Transcription regulation; DNA-binding; Nuclear protein; Repressor.
FT DNA_BIND 13 26 BASIC DOMAIN.
FT DOMAIN 27 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 139 148 PRO-RICH.
FT DOMAIN 154 157 WRPW MOTIF (REQUIRED FOR ACTIVITY)
FT (BY SIMILARITY).
SQ SEQUENCE 157 AA; 17028 MW; B5D621E814AE0369 CRC64;

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Query Match

Best Local Similarity 7.8%; Score 6; DB 1; Length 157;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 KRRRAR 68

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